

PCT09

RAW SEQUENCE LISTING

DATE: 11/12/2001

PATENT APPLICATION: US/09/744,989B

TIME: 18:27:48

Input Set : A:\P20637.SL2.ST25.txt

Output Set: N:\CRF3\11122001\I744989B.raw

3 <110> APPLICANT: Tsuganezawa, Keiko
 5 <120> TITLE OF INVENTION: Epimorphin of the Order Artiodactyla
 7 <130> FILE REFERENCE: P20637
 9 <140> CURRENT APPLICATION NUMBER: 09/744,989B
 10 <141> CURRENT FILING DATE: 1999-08-20
 12 <150> PRIOR APPLICATION NUMBER: JP 233892/1998
 13 <151> PRIOR FILING DATE: 1998-08-20
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04479
 16 <151> PRIOR FILING DATE: 1999-08-20
 18 <160> NUMBER OF SEQ ID NOS: 6
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 287
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Bos
 27 <400> SEQUENCE: 1
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 33 20 25 30
 35 Phe His Gln Val Glu Glu Ile Arg Asn Ser Ile Ala Lys Ile Ala Gln
 36 35 40 45
 38 Tyr Val Glu Glu Val Lys Lys Asn His Ser Ile Ile Leu Ser Ala Pro
 39 50 55 60
 41 Asn Pro Glu Gly Lys Ile Lys Glu Glu Leu Glu Asp Leu Asn Lys Glu
 42 65 70 75 80
 44 Ile Lys Lys Thr Ala Asn Lys Ile Arg Thr Lys Leu Lys Ser Ile Glu
 45 85 90 95
 47 Gln Ser Phe Asp Gln Asp Glu Gly Gly Asn Arg Thr Ser Val Glu Leu
 48 100 105 110
 50 Arg Ile Arg Arg Thr Gln His Ser Val Leu Ser Arg Lys Phe Val Glu
 51 115 120 125
 53 Val Met Thr Glu Tyr Asn Glu Ala Gln Thr Leu Phe Arg Glu Arg Ser
 54 130 135 140
 56 Lys Gly Arg Ile Gln Arg Gln Leu Glu Ile Thr Gly Lys Thr Thr Thr
 57 145 150 155 160
 59 Asp Asp Glu Leu Glu Glu Met Leu Glu Ser Gly Asn Pro Ser Ile Phe
 60 165 170 175
 62 Thr Ser Asp Ile Ile Ser Asp Ser Gln Ile Thr Arg Gln Ala Leu Asn
 63 180 185 190
 65 Glu Ile Glu Ser Arg His Lys Asp Ile Met Lys Leu Glu Thr Ser Ile
 66 195 200 205
 68 Arg Glu Leu His Glu Met Phe Met Asp Met Ala Met Phe Val Glu Thr
 69 210 215 220
 71 Gln Gly Glu Met Ile Asn Asn Ile Glu Lys Asn Val Met Asn Ala Ala
 72 225 230 235 240
 74 Asp Tyr Val Glu His Ala Lys Glu Glu Thr Lys Lys Ala Ile Lys Tyr

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75          245          250          255
77 Gln Ser Lys Ala Arg Arg Lys Met Met Phe Ile Ile Ile Cys Val Val
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80 Ile Leu Leu Val Ile Leu Gly Ile Ile Leu Ala Thr Thr Leu Ser
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84 <211> LENGTH: 864
85 <212> TYPE: DNA
86 <213> ORGANISM: Bos
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93 aacagtatag cgaaaatagc tcagtatgtc gaagaagtga agaaaaacca cagcatcatt      180
95 ctttctgcac caaacccaga aggaaaaata aaggaagagc ttgaagatct gaacaaagaa      240
97 atcaagaaaa ctgctaataa aataaggact aagttagaag ctattgaaca gagttttgat      300
99 caggatgagg gtggaaccg aacttctgtg gagcttcgga tacgaagaac ccagcattca      360
101 gtgctatctc gaaagtttgt ggaagtcagt acagaatata acgaagcaca gactctgttt      420
103 cgggagcgaa gcaaaggccg tatacagcgt cagctagaaa taactggaaa aactaccacc      480
105 gatgatgagc tggaagagat gctggaaagt gggaatccct ccatcttcac gtcagatatt      540
107 atatcagatt cacaaattac tagacaggct ctcaatgaaa ttgagtcccg tcataaagac      600
109 atcatgaagc tggagacaag catccgtgag ctacatgaga tgttcatgga catggccatg      660
111 ttcgtcgaga ctcagggtga aatgatcaac aacatagaaa aaaatgttat gaatgccgca      720
113 gactatgtag aacatgcaaa agaagaaacg aagaaagcta ttaaatatca aagcaaagca      780
115 agaaggaaaa tgatgttcat tattatttgt gtagttattt tgcttgtgat cettggaatt      840
117 atcctagcaa caacattgtc atag                                     864
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133 Phe His Gln Val Glu Glu Ile Arg Asn Ser Ile Ala Lys Ile Ala Gln
134          35          40          45
136 Tyr Val Glu Glu Val Lys Lys Asn His Ser Ile Ile Leu Ser Ala Pro
137          50          55          60
139 Asn Pro Glu Gly Lys Ile Lys Glu Glu Leu Glu Asp Leu Asn Lys Glu
140 65          70          75          80
142 Ile Lys Lys Thr Ala Asn Lys Ile Arg Thr Lys Leu Lys Ser Ile Glu
143          85          90          95
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146          100          105          110
148 Arg Ile Arg Arg Thr Gln His Ser Val Leu Ser Arg Lys Phe Val Glu
149          115          120          125
151 Val Met Thr Glu Tyr Asn Glu Ala Gln Thr Leu Phe Arg Glu Arg Ser
152          130          135          140
154 Lys Gly Arg Ile Gln Arg Gln Leu Glu Ile Thr Gly Lys Thr Thr Thr

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155 145                      150                      155                      160
157 Asp Asp Glu Leu Glu Glu Met Leu Glu Ser Gly Asn Pro Ser Ile Phe
158                      165                      170                      175
160 Thr Ser Asp Ile Ile Ser Asp Ser Gln Ile Thr Arg Gln Ala Leu Asn
161                      180                      185                      190
163 Glu Ile Glu Ser Arg His Lys Asp Ile Met Lys Leu Glu Thr Ser Ile
164                      195                      200                      205
166 Arg Glu Leu His Glu Met Phe Met Asp Met Ala Met Phe Val Glu Thr
167                      210                      215                      220
169 Gln Gly Glu Met Ile Asn Asn Ile Glu Lys Asn Val Met Asn Ala Ala
170 225                      230                      235                      240
172 Asp Tyr Val Glu His Ala Lys Glu Glu Thr Lys Lys Ala Ile Lys Tyr
173                      245                      250                      255
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188 aacagtatag cgaaaatagc tcagtatgtc gaagaagtga agaaaaacca cagcatcatt      180
190 ctttctgcac caaacccaga aggaaaaata aaggaagagc ttgaagatct gaacaaagaa      240
192 atcaagaaaa ctgctaataa aataaggact aagttgaagt ctattgaaca gagttttgat      300
194 caggatgagg gtggaaaccg aacttctgtg gagcttcgga tacgaagaac ccagcattca      360
196 gtgctatctc gaaagtttgt ggaagtcatg acagaatata acgaagcaca gactctgttt      420
198 cgggagcgaa gcaaaggccg tatacagcgt cagctagaaa taactggaaa aactaccacc      480
200 gatgatgagc tggagagatg gctggaaagt gggaatccct ccattcttcac gtcagatatt      540
202 atatcagatt cacaaattac tagacaggct ctcaatgaaa ttgagtcgccg tcataaagac      600
204 atcatgaagc tggagacaag catccgtgag ctacatgaga tgttcatgga catggccatg      660
206 ttcgtcgaga ctcagggtga aatgatcaac aacatagaaa aaaatgttat gaatgccgca      720
208 gactatgtag aacatgcaaa agaagaaacg aagaaagcta ttaaataatca aagcaaagca      780
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214 <211> LENGTH: 287
215 <212> TYPE: PRT
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223 Gly Asp Thr Thr Val Val Val Glu Lys Asp His Phe Met Asp Asp Phe
224                      20                      25                      30
226 Phe His Gln Val Glu Glu Ile Arg Asn Ser Ile Ala Lys Ile Ala Gln
227                      35                      40                      45
229 Tyr Val Glu Glu Val Lys Lys Asn His Ser Ile Ile Leu Ser Ala Pro
230                      50                      55                      60
232 Asn Pro Glu Gln Lys Ile Lys Glu Glu Leu Glu Asp Leu Asn Lys Glu
233 65                      70                      75                      80

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235 Ile Lys Lys Thr Ala Asn Lys Ile Arg Thr Lys Leu Lys Ser Ile Glu
236           85           90           95
238 Gln Ser Phe Asp Gln Asp Glu Gly Gly Asn Arg Thr Ser Val Glu Leu
239           100           105           110
241 Arg Ile Arg Arg Thr Gln His Ser Val Leu Ser Arg Lys Phe Val Glu
242           115           120           125
244 Val Met Thr Glu Phe Asn Glu Ala Gln Thr Leu Phe Arg Glu Arg Ser
245           130           135           140
247 Lys Gly Arg Ile Gln Arg Gln Leu Glu Ile Thr Gly Lys Thr Thr Thr
248 145           150           155           160
250 Asp Asp Glu Leu Glu Glu Met Leu Glu Ser Gly Asn Pro Ser Ile Phe
251           165           170           175
253 Thr Ser Asp Ile Ile Ser Asp Ser Gln Ile Thr Arg Gln Ala Leu Asn
254           180           185           190
256 Glu Ile Glu Ser Arg His Lys Asp Ile Met Lys Leu Glu Thr Ser Ile
257           195           200           205
259 Arg Glu Leu His Glu Met Phe Met Asp Met Ala Met Phe Val Glu Thr
260           210           215           220
262 Gln Gly Glu Met Ile Asn Asn Ile Glu Lys Asn Val Thr Asn Ala Ala
263 225           230           235           240
265 Asp Tyr Val Glu His Ala Lys Glu Glu Thr Lys Lys Ala Ile Lys Tyr
266           245           250           255
268 Gln Ser Lys Ala Arg Arg Lys Met Met Phe Ile Ile Ile Cys Val Val
269           260           265           270
271 Ile Leu Leu Val Ile Phe Gly Ile Ile Leu Ala Thr Thr Leu Ser
272           275           280           285

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274 <210> SEQ ID NO: 6

275 <211> LENGTH: 864

276 <212> TYPE: DNA

277 <213> ORGANISM: Ovis

279 <400> SEQUENCE: 6

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286 ctttctgcac caaaccgaga aggaaaaata aaggaagagc ttgaagatct gaacaaagaa      240
288 atcaagaaaa ctgccataaa aattcggact aagttgaagt ctattgaaca gagttttgat      300
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302 ttcgtcgaga ccaggggtga aatgatcaac aacatagaaa aaaatgttac gaatgccgca      720
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308 atcctagcaa caacattgtc atag                                     864

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